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26 JUL 2007

LAW OFFICES OF KARL HORMANN
P.O. BOX 381516
CAMBRIDGE, MA 02238-1516

In re Application of MOCK et al :
U.S. Application No.: 10/528,708 :
PCT Application No.: PCT/DE2003/003180 :
Int. Filing Date: 21 September 2003 : DECISION
Priority Date Claimed: 22 September 2002 :
Attorney Docket No.: 050677-US :
For: NUCLEIC ACID SEQUENCES CODING :
FOR PROTEOLYTIC ENZYMES ... :

This is in response to applicant's "Enquiry" filed 27 June 2007, which is being treated as a petition to withdraw a holding of abandonment under 37 CFR 1.181. No petition fee is due.

BACKGROUND

On 21 September 2003, applicant filed international application PCT/DE2003/003180, which claimed priority of an earlier Germany application filed 22 September 2002. A copy of the international application was communicated to the USPTO from the International Bureau on 08 April 2004. The thirty-month period for paying the basic national fee in the United States expired on 22 March 2005.

On 22 March 2005, applicant filed national stage papers in the United States Designated/Elected Office (DO/EO/US). The submission was accompanied by, *inter alia*, the basic national fee required by 35 U.S.C. 371(c)(1).

On 24 October 2005, the DO/EO/US mailed a Notification to Comply with Requirements for Patent Applications Containing Nucleotide and/or Amino Acid Sequence Disclosures (Form PCT/DO/EO/922)¹, which indicated that a substitute sequence listing in computer readable form must be furnished.

On 07 December 2006, the DO/EO/US mailed a Notification of Abandonment (Form PCT/DO/EO/909)², which indicated that the application is abandoned for failure to timely respond to the Notification to Comply mailed 24 October 2005.

¹ Copy attached.

² Copy attached.

On 27 June 2007, applicant filed the present petition under 37 CFR 1.181.

DISCUSSION

MPEP 403 states in relevant part:

37 CFR 1.33(a) provides that in a patent application the applicant must specify a correspondence address to which the Office will send notices, letters and other communications relating to the application. The correspondence address must appear either in an application data sheet (37 CFR 1.76) or in a clearly identifiable manner elsewhere in any papers submitted with an application filing. Where more than one correspondence address is specified, the Office will **>select one of the correspondence addresses for use< as the correspondence address. This is intended to cover, for example, the situation where an application is submitted with multiple addresses, such as one correspondence address being given in the application transmittal letter, and a different one in an accompanying 37 CFR 1.63 oath or declaration, or other similar situations. The **>Office will select which of the multiple correspondence addresses to use according to the following order: (A) application data sheet (ADS); (B) application transmittal; (C) oath or declaration (unless power of attorney is more current); and (D) power of attorney.< If more than one correspondence address is specified in a single document, the Office will *>select< the address associated with a Customer Number over a typed correspondence address.

A review of the application file reveals that the national stage papers filed on 22 March 2005 were submitted with multiple addresses. In particular, the transmittal letter (Form PTO-1390) specified the correspondence address as "Law Offices of Karl Hormann, P.O. Box 381516, Cambridge, MA 02238-1516", whereas the express mail certificate listed Customer Number 30234. The mailing address associated with Customer Number 30234 is "Law Offices of Karl Hormann, 86 Sparks Street, Cambridge, MA 02138".

The Notification to Comply and the Notification of Abandonment were mailed to the address associated with Customer Number 30234. In accordance with MPEP 403, the mailing address on the transmittal letter (Form PTO-1390) should have been selected as the correspondence address.

Applicant is advised that a Request for Customer Number Data Change (Form PTO/SB/124) may be used to change the address associated with an existing Customer Number.

CONCLUSION

For the reasons above, the petition under 37 CFR 1.181 is GRANTED.

The Notification of Abandonment (Form PCT/DO/EO/909) mailed 07 December 2006 is hereby VACATED.

A proper response to the Notification to Comply with Requirements for Patent Applications Containing Nucleotide and/or Amino Acid Sequence Disclosures (Form PCT/DO/EO/922), must be filed within TWO (2) MONTHS from the mail date of this decision. Failure to timely file a proper response will result in ABANDONMENT of the application. Extensions of time are available under 37 CFR 1.136(a).

This application is being forwarded to the United States Designated/Elected Office (DO/EO/US) for further processing in accordance with this decision.



Bryan Lin
PCT Legal Examiner
PCT Legal Office

Telephone: 571-272-3303
Facsimile: 571-273-0459

ATTACHMENTS:

1. copy of Notification to Comply with Requirements for Patent Applications Containing Nucleotide and/or Amino Acid Sequence Disclosures (Form PCT/DO/EO/922)³
2. copy of Notification of Abandonment (Form PCT/DO/EO/909)⁴

³ Response outstanding.

⁴ Vacated by this decision.



UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE
 United States Patent and Trademark Office
 Address: COMMISSIONER FOR PATENTS
 P.O. Box 1430
 Alexandria, Virginia 22313-1430
 www.uspto.gov

U.S. APPLICATION NUMBER NO.	FIRST NAMED APPLICANT	ATTY. DOCKET NO.
10/528,708	Thomas Mock	050677-US

30234
 LAW OFFICES OF KARL HORMANN
 86 SPARKS STREET
 CAMBRIDGE, MA 02138

INTERNATIONAL APPLICATION NO.	
PCT/DE03/03180	
I.A. FILING DATE	PRIORITY DATE
09/21/2003	09/22/2002

CONFIRMATION NO. 9380
 371 FORMALITIES LETTER



Date Mailed: 10/24/2005

NOTIFICATION TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant is given **TWO MONTHS FROM THE DATE OF THIS NOTICE** within which to file the items indicated below to avoid abandonment. Extensions of time may be obtained under the provisions of 37 CFR 1.136(a).

- A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing." Applicant must provide a substitute computer readable form (CRF) copy of the "Sequence Listing" and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d).

Applicant is cautioned that correction of the above items may cause the specification and drawings page count to exceed 100 pages. If the specification and drawings exceed 100 pages, applicant will need to submit the required application size fee.

For questions regarding compliance to 37 CFR 1.821-1.825 requirements, please contact:

- For Rules Interpretation, call (571) 272-0951
- For Patentin Software Program Help, call Patent EBC at 1-866-217-9197 or directly at 703-305-3028 / 703-308-6845 between the hours of 6 a.m. and 12 midnight, Monday through Friday, EST.
- Send e-mail correspondence for Patentin Software Program Help @ ebc@uspto.gov

Applicant is reminded that any communications to the United States Patent and Trademark Office must be mailed to the address given in the heading and include the U.S. application no. shown above (37 CFR 1.5)

*A copy of this notice **MUST** be returned with the response.*

JOHN L ANDERSON

Telephone: (703) 308-9140 EXT 211

PART 2 - OFFICE COPY

U.S. APPLICATION NUMBER NO.	INTERNATIONAL APPLICATION NO.	ATTY. DOCKET NO.
10/528,708	PCT/DE03/03180	050677-US

FORM PCT/DO/EO/922 (371 Formalities Notice)

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/528,708
Source: PJ
Date Processed by STIC: 3/30/05

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.2.2 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail. Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom. Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

- 1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)**
- 2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
- 3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314**

Revised 01/24/05

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Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/528,708

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☒ **Wrapped Nucleics
Wrapped Aminos** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☐ **Misaligned Amino
Numbering** The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☒ **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ **Variable Length** Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ **PatentIn 2.0
"bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ **Skipped Sequences
(OLD RULES)** Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ **Skipped Sequences
(NEW RULES)** Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 ☐ **Use of n's or Xaa's
(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 ☐ **Invalid <213>
Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ **Use of <220>** Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ **PatentIn 2.0
"bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ **Misuse of n/Xaa** "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid

AMC - Biotechnology Systems Branch - 09/09/2003

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PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/528,708

DATE: 03/30/2005
TIME: 14:13:00

Input Set : A:\PTO.SR.txt
Output Set: N:\CRF4\03302005\J528708.raw

3 <110> APPLICANT: Stiftung Alfred-Wegener-Institut fuer Polar- und
4 Meeresforschung,
5 Bremerhaven, Germany
7 <120> TITLE OF INVENTION: A novel nucleic acid sequence coding for a calpain
8 protease from the coldness-adapted marine fragilariopsis
9 cylindrus diatom
11 <130> FILE REFERENCE: AWI 01/0902 DE
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/528,708
C--> 13 <141> CURRENT FILING DATE: 2005-03-22
13 <160> NUMBER OF SEQ ID NOS: 4

ERRORED SEQUENCES

15 <210> SEQ ID NO: 1
16 <211> LENGTH: 544
17 <212> TYPE: DNA
18 <213> ORGANISM: Fragilariopsis cylindrus
20 <400> SEQUENCE: 1
E--> 22 gg gaa ttc ggc ctt acg gcc ggg gat gat gga atg ttc tgg att
23 agt 47
24 Glu Phe Gly Leu Thr Ala Gly Asp Asp Gly Met Phe Trp Ile
W--> 25 Ser
W--> 26 1 5 10
E--> 27 15
E--> 29 tgg gag gat gtc ttg ctt tat ttc cgc aat tta caa tta tca tgg
30 aat 95
31 Trp Glu Asp Val Leu Leu Tyr Phe Arg Asn Leu Gln Leu Ser Trp
W--> 32 Asn
W--> 33 20 25 30
E--> 35 ccc aaa cta ttt gcg tat cgg atg act act cat ggc tta tgg cca
36 aag 143
37 Pro Lys Leu Phe Ala Tyr Arg Met Thr Thr His Gly Leu Trp Pro
W--> 38 Lys
W--> 39 35 40 45
E--> 41 gat cag gga cca caa aat gat gca ttt aat gtc gga gag aat cca
42 caa 191
43 Asp Gln Gly Pro Gln Asn Asp Ala Phe Asn Val Gly Glu Asn Pro
W--> 44 Gln
W--> 45 50 55 60
E--> 47 tat atc atg tct ttc tcc gaa aaa gct gta tcg agt aaa cca acg
48 att 239
49 Tyr Ile Met Ser Phe Ser Glu Lys Ala Val Ser Ser Lys Pro Thr

Does Not Comply
Corrected Diskette Needed

see item 1
on Error
summary
sheet

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/528,708

DATE: 03/30/2005
 TIME: 14:13:00

Input Set : A:\PTO.SR.txt
 Output Set: N:\CRF4\03302005\J528708.raw

```

W--> 50 Ile
W--> 51      65              70              75
E--> 53 tgg gta ctg ata tca agg cat gta agc aaa cag gag caa gaa ggt
54 gct      287
55 Trp Val Leu Ile Ser Arg His Val Ser Lys Gln Glu Gln Glu Gly
W--> 56 Ala
W--> 57 80              85              90
E--> 58 95
E--> 60 gag gtg aat gat ttc tta acc ata cat ctc gtt aga aac tcg gct
61 aca      335
62 Glu Val Asn Asp Phe Leu Thr Ile His Leu Val Arg Asn Ser Ala
W--> 63 Thr
W--> 64      100              105              110
E--> 66 tta gaa aga gtt tgg tat ccc cat gga aaa gca acg att gct aat
67 gga      383
68 Leu Glu Arg Val Trp Tyr Pro His Gly Lys Ala Thr Ile Ala Asn
W--> 69 Gly
W--> 72      115              120              125
E--> 74 tgc tat aca aac aat cca cac gtg ctt tta cga tac gat gtt tcc
75 gga      431
76 Cys Tyr Thr Asn Asn Pro His Val Leu Leu Arg Tyr Asp Val Ser
W--> 77 Gly
W--> 78      130              135              140
E--> 80 cct gaa gat caa ttt atc tcg tta gta ctg tct caa cac gaa aaa
81 act      479
82 Pro Glu Asp Gln Phe Ile Ser Leu Val Leu Ser Gln His Glu Lys
W--> 83 Thr
W--> 84      145              150              155
E--> 86 caa gat cta tca tac act ctc tct tgt tac tgt acc gaa ccc ttt
87 aca      527
88 Gln Asp Leu Ser Tyr Thr Leu Ser Cys Tyr Cys Thr Glu Pro Phe
W--> 89 Thr
W--> 90 160              165              170
E--> 91 175
E--> 93 cta gga aga cca cca aa
94      544
95 Leu Gly Arg Pro Pro
W--> 96      180
99 <210> SEQ ID NO: 2
100 <211> LENGTH: 180
101 <212> TYPE: DNA
102 <213> ORGANISM: Fragilariopsis cylindrus
104 <400> SEQUENCE: 2
105      Glu Phe Gly Leu Thr Ala Gly Asp Asp Gly Met Phe Trp Ile
W--> 106 Ser
W--> 107      1              5              10
E--> 108 15
110 Trp Glu Asp Val Leu Leu Tyr Phe Arg Asn Leu Gln Leu Ser Trp
W--> 111 Asn

```

*see item 1
on Error
summary sheet*

see item 1

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/528,708

DATE: 03/30/2005
TIME: 14:13:00

Input Set : A:\PTO.SR.txt
Output Set: N:\CRF4\03302005\J528708.raw

```

W--> 112          20          25          30
      114 Pro Lys Leu Phe Ala Tyr Arg Met Thr Thr His Gly Leu Trp Pro
W--> 115 Lys
W--> 116          35          40          45
      118 Asp Gln Gly Pro Gln Asn Asp Ala Phe Asn Val Gly Glu Asn Pro
W--> 119 Gln
W--> 120          50          55          60
      122 Tyr Ile Met Ser Phe Ser Glu Lys Ala Val Ser Ser Lys Pro Thr
W--> 123 Ile
W--> 124          65          70          75
      126 Trp Val Leu Ile Ser Arg His Val Ser Lys Gln Glu Gln Glu Gly
W--> 127 Ala
W--> 128 80          85          90
E--> 129 95
      131 Glu Val Asn Asp Phe Leu Thr Ile His Leu Val Arg Asn Ser Ala
W--> 132 Thr
W--> 133          100          105          110
      135 Leu Glu Arg Val Trp Tyr Pro His Gly Lys Ala Thr Ile Ala Asn
W--> 136 Gly
W--> 137          115          120          125
      141 Cys Tyr Thr Asn Asn Pro His Val Leu Leu Arg Tyr Asp Val Ser
W--> 142 Gly
W--> 143          130          135          140
      145 Pro Glu Asp Gln Phe Ile Ser Leu Val Leu Ser Gln His Glu Lys
W--> 146 Thr
W--> 147          145          150          155
      149 Gln Asp Leu Ser Tyr Thr Leu Ser Cys Tyr Cys Thr Glu Pro Phe
W--> 150 Thr
W--> 151 160          165          170
E--> 152 175
      154 Leu Gly Arg Pro Pro
E--> 155          180
      159 <210> SEQ ID NO: 3
      160 <211> LENGTH: 544
      161 <212> TYPE: DNA
      162 <213> ORGANISM: Fragilariopsis cylindrus
      164 <400> SEQUENCE: 3
E--> 166 tca aac gat ggt gcg caa tac gta gta gag aaa tog ata ctg gta
      167 ggt 48
      168 Ser Asn Asp Gly Ala Gln Tyr Val Val Glu Lys Ser Ile Leu Val
W--> 169 Gly
W--> 170 1          5          10          15
E--> 172 tca gtg aat tat cct gta aaa gat cca ttt aat cag atg aaa cgt
      173 gga 96
      174 Ser Val Asn Tyr Pro Val Lys Asp Pro Phe Asn Gln Met Lys Arg
W--> 175 Gly
W--> 176          20          25          30
E--> 178 tca ctt caa acc tac tca gat tca tgg acc gaa cgg gat cgt acc
      179 tca 144

```

see item 1

see item 1

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/528,708

DATE: 03/30/2005
TIME: 14:13:00

Input Set : A:\PTO.SR.txt
Output Set: N:\CRF4\03302005\J528708.raw

```

180 Ser Leu Gln Thr Tyr Ser Asp Ser Trp Thr Glu Arg Asp Arg Thr
W--> 181 Ser
W--> 182          35          40          45
E--> 184 ttt gtc atg gca tca cgt aac tta gcc gat ttt cgt aat aac gtg
185 aag 192
186 Phe Val Met Ala Ser Arg Asn Leu Ala Asp Phe Arg Asn Asn Val
W--> 187 Lys
W--> 188          50          55          60
E--> 190 gta aag atc gat got gtt ttt aat cca ott ttt atc aac gag gaa
191 tac 240
192 Val Thr Ile Asp Ala Val Phe Asn Pro Leu Phe Ile Asn Glu Glu
W--> 193 Tyr
W--> 194 65          70          75
E--> 195 80
E--> 197 aaa tgg atc ttt cgt caa gaa ggc tgg agg tta gag aca cct gac
198 aat 288
199 Lys Trp Ile Phe Arg Gln Glu Gly Trp Arg Leu Glu Thr Pro Asp
W--> 200 Asn
W--> 201          85          90          95
E--> 203 gtc aac cta ott atc aat ggg aac gct tat gta aac got aag gcc
204 gac 336
205 Val Asn Leu Leu Ile Asn Gly Asn Ala Tyr Val Asn Ala Lys Ala
W--> 206 Asp
W--> 207          100          105          110
E--> 211 cag atg gac ccc caa gag gtt atg ata aag caa atc tac agc aat
212 ctc 384
213 Gln Met Asp Pro Gln Glu Val Met Ile Lys Gln Ile Tyr Ser Asn
W--> 214 Leu
W--> 215          115          120          125
E--> 217 ttt gct gat cac gtg tat agc aaa agt cca aaa gga gac gcc gcc
218 caa 432
219 Phe Ala Asp His Val Tyr Ser Lys Ser Pro Lys Gly Asp Ala Ala
W--> 220 Gln
W--> 221          130          135          140
E--> 223 gta gtc acc atg aca ttg gca cca agg gcg aat tct gca gat atc
224 cat 480
225 Val Val Thr Met Thr Leu Ala Pro Arg Ala Asn Ser Ala Asp Ile
W--> 226 His
W--> 227 145          150          155
E--> 228 160
E--> 230 cac act ggc ggc cgt ctc gag cat gca tct aga ggg ccc aat tcg
231 ccc 528
232 His Thr Gly Gly Arg Leu Glu His Ala Ser Arg Gly Pro Asn Ser
W--> 233 Pro
W--> 234          165          170          175
E--> 236 tat agt gag tcg tat t
237 544
238 Tyr Ser Glu Ser Tyr
W--> 239          180 181

```

*see
item 1*

*← delete (insert amino acid number
under every 5 amino acids)*

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/10/528,708

DATE: 03/30/2005
 TIME: 14:13:00

Input Set : A:\PTO.SR.txt
 Output Set: N:\CRF4\03302005\J528708.raw

242 <210> SEQ ID NO: 4
 243 <211> LENGTH: 181
 244 <212> TYPE: DNA
 245 <213> ORGANISM: Fragilariaopsis cylindrus
 247 <400> SEQUENCE: 4
 249 Ser Asn Asp Gly Ala Gln Tyr Val Val Glu Lys Ser Ile Leu Val
 W--> 250 Gly
 W--> 251 1 5 10 15
 253 Ser Val Asn Tyr Pro Val Lys Asp Pro Phe Asn Gln Met Lys Arg
 W--> 254 Gly
 W--> 255 20 25 30
 257 Ser Leu Gln Thr Tyr Ser Asp Ser Trp Thr Glu Arg Asp Arg Thr
 W--> 258 Ser
 W--> 259 35 40 45
 261 Phe Val Met Ala Ser Arg Asn Leu Ala Asp Phe Arg Asn Asn Val
 W--> 262 Lys
 W--> 263 50 55 60
 265 Val Thr Ile Asp Ala Val Phe Asn Pro Leu Phe Ile Asn Glu Glu
 W--> 266 Tyr
 W--> 267 65 70 75
 E--> 268 80
 270 Lys Trp Ile Phe Arg Gln Glu Gly Trp Arg Leu Glu Thr Pro Asp
 W--> 271 Asn
 W--> 272 85 90 95
 274 Val Asn Leu Leu Ile Asn Gly Asn Ala Tyr Val Asn Ala Lys Ala
 W--> 275 Asp
 W--> 276 100 105 110
 280 Gln Met Asp Pro Gln Glu Val Met Ile Lys Gln Ile Tyr Ser Asn
 W--> 281 Leu
 W--> 282 115 120 125
 284 Phe Ala Asp His Val Tyr Ser Lys Ser Pro Lys Gly Asp Ala Ala
 W--> 285 Gln
 W--> 286 130 135 140
 288 Val Val Thr Met Thr Leu Ala Pro Arg Ala Asn Ser Ala Asp Ile
 W--> 289 His
 W--> 290 145 150 155
 E--> 291 160
 293 His Thr Gly Gly Arg Leu Glu His Ala Ser Arg Gly Pro Asn Ser
 W--> 294 Pro
 W--> 295 165 170 175
 297 Tyr Ser Glu Ser Tyr
 W--> 298 180 181
 E--> 301 ~~Attorney-Doctet 050677-US~~

*see
 item 1*

delete

see p. 6 for more errors

10/528,708 6

Sequence Protocol

Listing

<110>Stiftung Alfred-Wegener-Institut fuer Polar- und
Meeresforschung.
Bremerhaven, Germany

<120>A novel nucleic acid sequence coding for a calpain
protease from the coldness-adapted marine fragilariopsis
cylindrus diatom

do not
use
italics

use a
fixed-width font

only

(per 1.823 of Sequence Rules)

BEST AVAILABLE COPY

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/528,708

DATE: 03/30/2005
TIME: 14:13:01

Input Set : A:\PTO.SR.txt
Output Set: N:\CRF4\03302005\J528708.raw

L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:22 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:44 SEQ:1
L:25 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:26 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
M:254 Repeated in SeqNo=1
L:32 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:33 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:38 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:39 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:44 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:45 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:50 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:51 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:56 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:57 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:63 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:64 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:69 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:72 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:77 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:78 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:83 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:84 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:89 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:90 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:96 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:106 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:107 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:108 M:254 E: No. of Bases conflict, this line has no nucleotides.
L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:112 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:115 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:116 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:119 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:120 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:123 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:124 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:127 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:128 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
M:254 Repeated in SeqNo=2
L:132 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:133 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:136 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:137 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:142 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:143 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
L:146 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/528,708

DATE: 03/30/2005

TIME: 14:13:01

Input Set : A:\PTO.SR.txt

Output Set: N:\CRF4\03302005\J528708.raw

L:147 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
 L:150 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
 L:151 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
 L:155 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:2
 L:155 M:301 E: (44) No Sequence Data was Shown, SEQ ID:2
 L:155 M:252 E: No. of Seq. differs, <211> LENGTH:Input:180 Found:0 SEQ:2
 L:166 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:45 SEQ:3
 L:169 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:170 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 M:254 Repeated in SeqNo=3
 L:175 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:176 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3
 L:268 M:254 E: No. of Bases conflict, this line has no nucleotides.
 M:254 Repeated in SeqNo=4
 L:301 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:3
 L:301 M:301 E: (44) No Sequence Data was Shown, SEQ ID:4
 L:301 M:252 E: No. of Seq. differs, <211> LENGTH:Input:181 Found:0 SEQ:4



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10/528,708	Thomas Mock	050677-US

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30234
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CONFIRMATION NO. 9380

371
 ABANDONMENT/TERMINATION
 LETTER



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Date Mailed: 12/07/2006

NOTIFICATION OF ABANDONMENT

The United States Patent and Trademark Office in its capacity as a Designated / Elected Office (37 CFR 1.495) has made the following determination:

- Applicant has failed to respond to the notification of MISSING REQUIREMENTS (Form PCT/DO/EO/905), mailed 10/24/2005 within the time period set therein.

Therefore, the above identified application failed to meet the requirements of 35 U.S.C. 371 and 37 CFR 1.495, and is ABANDONED AS TO THE UNITED STATES OF AMERICA.

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PART 3 - OFFICE COPY

FORM PCT/DO/EO/909 (371 Abandonment Notice)